

Does Not Comply
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/091,342

DATE: 11/12/2002
TIME: 10:35:58

Input Set : A:\pto.vsk.txt
Output Set: N:\CRF4\11122002\J091342.raw

W--> 1 SEQUENZPROTOKOLL ← remove

3 <110> APPLICANT: Degussa AG
4 National University of Ireland, Galway
5 Forschungszentrum Julich GmbH
7 <120> TITLE OF INVENTION: Process for the fermentative Preparation of L-Amino Acids
with
8 Amplification of the zwf Gene.
10 <130> FILE REFERENCE: 990239BT
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/091,342
C--> 13 <141> CURRENT FILING DATE: 2002-03-06
15 <160> NUMBER OF SEQ ID NOS: 20
17 <170> SOFTWARE: PatentIn Ver. 2.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 2811
21 <212> TYPE: DNA
22 <213> ORGANISM: Corynebacterium glutamicum
24 <220> FEATURE:
25 <221> NAME/KEY: CDS
26 <222> LOCATION: (373)..(2022)
27 <223> OTHER INFORMATION: pgi
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34 aaaagggggc cgggttcaaa ttcccaaaaa aaatggcaaa aaagggggggg ccaaaaaccaa 180
36 gttggccccc aaaccaccgg ggcaacggcc caccacaaaa ggggttgggt taaaggaagg 240
38 acgccccaaag taagcccga atggcccacg ttcgaaaaag caggccccaa ttaaaccgcac 300
40 cttaaatttg tcgtgtttcc cactttgaac actcttcgat gcgcttggcc acaaaagcaa 360
42 gctaacctga ag atg tta ttt aac gac aat aaa gga gtt ttc atg gcg gac 411
43 Met Leu Phe Asn Asp Asn Lys Gly Val Phe Met Ala Asp
44 1 5 10
46 att tcg acc acc cag gtt tgg caa gac ctg acc gat cat tac tca aac 459
47 Ile Ser Thr Thr Gln Val Trp Gln Asp Leu Thr Asp His Tyr Ser Asn
48 15 20 25
50 ttc cag gca acc act ctg cgt gaa ctt ttc aag gaa gaa aac cgc gcc 507
51 Phe Gln Ala Thr Thr Leu Arg Glu Leu Phe Lys Glu Glu Asn Arg Ala
52 30 35 40 45
54 gag aag tac acc ttc tcc gcg gct ggc ctc cac gtc gac ctg tcg aag 555
55 Glu Lys Tyr Thr Phe Ser Ala Ala Gly Leu His Val Asp Leu Ser Lys
56 50 55 60
58 aat ctg ctt gac gac gcc acc ctc acc aag ctc ctt gca ctg acc gaa 603
59 Asn Leu Leu Asp Asp Ala Thr Leu Thr Lys Leu Leu Ala Leu Thr Glu
60 65 70 75
62 gaa tct ggc ctt cgc gaa cgc att gac gcg atg ttt gcc ggt gaa cac 651
63 Glu Ser Gly Leu Arg Glu Arg Ile Asp Ala Met Phe Ala Gly Glu His

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64	80	85	90	
66	ctc aac aac acc gaa gac cgc gct gtc ctc cac acc gcg ctg cgc ctt	699		
67	Leu Asn Asn Thr Glu Asp Arg Ala Val Leu His Thr Ala Leu Arg Leu			
68	95 100 105			
70	cct gcc gaa gct gat ctg tca gta gat ggc caa gat gtt gct gct gat	747		
71	Pro Ala Glu Ala Asp Leu Ser Val Asp Gly Gln Asp Val Ala Ala Asp			
72	110 115 120 125			
74	gtc cac gaa gtt ttg gga cgc atg cgt gac ttc gct act gcg ctg cgc	795		
75	Val His Glu Val Leu Gly Arg Met Arg Asp Phe Ala Thr Ala Leu Arg			
76	130 135 140			
78	tca ggc aac tgg ttg gga cac acc ggc cac acg atc aag aag atc gtc	843		
79	Ser Gly Asn Trp Leu Gly His Thr Gly His Thr Ile Lys Lys Ile Val			
80	145 150 155			
82	aac att ggt atc ggt ggc tct gac ctc gga cca gcc atg gct acg aag	891		
83	Asn Ile Gly Ile Gly Gly Ser Asp Leu Gly Pro Ala Met Ala Thr Lys			
84	160 165 170			
86	gct ctg cgt gca tac gcg acc gct ggt atc tca gca gaa ttc gtc tcc	939		
87	Ala Leu Arg Ala Tyr Ala Thr Ala Gly Ile Ser Ala Glu Phe Val Ser			
88	175 180 185			
90	aac gtc gac cca gca gac ctc gtt tct gtg ttg gaa gac ctc gat gca	987		
91	Asn Val Asp Pro Ala Asp Leu Val Ser Val Leu Glu Asp Leu Asp Ala			
92	190 195 200 205			
94	gaa tcc aca ttg ttc gtg atc gct tcg aaa act ttc acc acc cag gag	1035		
95	Glu Ser Thr Leu Phe Val Ile Ala Ser Lys Thr Phe Thr Thr Gln Glu			
96	210 215 220			
98	acg ctg tcc aac gct cgt gca gct cgt gct tgg ctg gta gag aag ctc	1083		
99	Thr Leu Ser Asn Ala Arg Ala Ala Arg Ala Trp Leu Val Glu Lys Leu			
100	225 230 235			
102	ggt gaa gag gct gtc gcg aag cac ttc gtc gca gtg tcc acc aat gct	1131		
103	Gly Glu Glu Ala Val Ala Lys His Phe Val Ala Val Ser Thr Asn Ala			
104	240 245 250			
106	gaa aag gtc gca gag ttc ggt atc gac acg gac aac atg ttc ggc ttc	1179		
107	Glu Lys Val Ala Glu Phe Gly Ile Asp Thr Asp Asn Met Phe Gly Phe			
108	255 260 265			
110	tgg gac tgg gtc gga ggt cgt tac tcc gtg gac tcc gca gtt ggt ctt	1227		
111	Trp Asp Trp Val Gly Gly Arg Tyr Ser Val Asp Ser Ala Val Gly Leu			
112	270 275 280 285			
114	tcc ctc atg gca gtg atc ggc cct cgc gac ttc atg cgt ttc ctc ggt	1275		
115	Ser Leu Met Ala Val Ile Gly Pro Arg Asp Phe Met Arg Phe Leu Gly			
116	290 295 300			
118	gga ttc cac gcg atg gat gaa cac ttc cgc acc acc aag ttc gaa gag	1323		
119	Gly Phe His Ala Met Asp Glu His Phe Arg Thr Thr Lys Phe Glu Glu			
120	305 310 315			
122	aac gtt cca atc ttg atg gct ctg ctc ggt gtc tgg tac tcc gat ttc	1371		
123	Asn Val Pro Ile Leu Met Ala Leu Leu Gly Val Trp Tyr Ser Asp Phe			
124	320 325 330			
126	tat ggt gca gaa acc cac gct gtc cta cct tat tcc gag gat ctc agc	1419		
127	Tyr Gly Ala Glu Thr His Ala Val Leu Pro Tyr Ser Glu Asp Leu Ser			
128	335 340 345			

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130 cgt ttt gct gct tac ctc cag cag ctg acc atg gag acc aat ggc aag 1467
131 Arg Phe Ala Ala Tyr Leu Gln Gln Leu Thr Met Glu Thr Asn Gly Lys
132 350 355 360 365
134 tca gtc cac cgc gac ggc tcc cct gtt tcc act ggc act ggc gaa att 1515
135 Ser Val His Arg Asp Gly Ser Pro Val Ser Thr Gly Thr Gly Glu Ile
136 370 375 380
138 tac tgg ggt gag cct ggc aca aat ggc cag cac gct ttc ttc cag ctg 1563
139 Tyr Trp Gly Glu Pro Gly Thr Asn Gly Gln His Ala Phe Phe Gln Leu
140 385 390 395
142 atc cac cag ggc act cgc ctt gtt cca gct gat ttc att ggt ttc gct 1611
143 Ile His Gln Gly Thr Arg Leu Val Pro Ala Asp Phe Ile Gly Phe Ala
144 400 405 410
146 cgt cca aag cag gat ctt cct gcc ggt gag cgc acc atg cat gac ctt 1659
147 Arg Pro Lys Gln Asp Leu Pro Ala Gly Glu Arg Thr Met His Asp Leu
148 415 420 425
150 ttg atg agc aac ttc ttc gca cag acc aag gtt ttg gct ttc ggt aag 1707
151 Leu Met Ser Asn Phe Phe Ala Gln Thr Lys Val Leu Ala Phe Gly Lys
152 430 435 440 445
154 aac gct gaa gag atc gct gcg gaa ggt gtc gca cct gag ctg gtc aac 1755
155 Asn Ala Glu Glu Ile Ala Ala Glu Gly Val Ala Pro Glu Leu Val Asn
156 450 455 460
158 cac aag gtc gtg cca ggt aat cgc cca acc acc acc att ttg gcg gag 1803
159 His Lys Val Val Pro Gly Asn Arg Pro Thr Thr Thr Ile Leu Ala Glu
160 465 470 475
162 gaa ctt acc cct tct att ctc ggt gcg ttg atc gct ttg tac gaa cac 1851
163 Glu Leu Thr Pro Ser Ile Leu Gly Ala Leu Ile Ala Leu Tyr Glu His
164 480 485 490
166 acc gtg atg gtt cag ggc gtg att tgg gac atc aac tcc ttc gac caa 1899
167 Thr Val Met Val Gln Gly Val Ile Trp Asp Ile Asn Ser Phe Asp Gln
168 495 500 505
170 tgg ggt gtt gaa ctg ggc aaa cag cag gca aat gac ctc gct ccg gct 1947
171 Trp Gly Val Glu Leu Gly Lys Gln Gln Ala Asn Asp Leu Ala Pro Ala
172 510 515 520 525
174 gtc tct ggt gaa gag gat gtt gac tcg gga gat tct tcc act gat tca 1995
175 Val Ser Gly Glu Glu Asp Val Asp Ser Gly Asp Ser Ser Thr Asp Ser
176 530 535 540
178 ctg att aag tgg tac cgc gca aat agg tagtcgcttg cttatagggt 2042
179 Leu Ile Lys Trp Tyr Arg Ala Asn Arg
180 545 550
182 caggggcgtg aagaatcctc gcctcatagc actggccgct atcatcctga cctcgttcaa 2102
184 tctgcgaaca gctattactg ctttagctcc gctggtttct gagattcggg atgatttagg 2162
186 ggtagtgct tctcttattg gtgtgttggg catgatcccg actgctatgt tcgcggttgc 2222
188 tgcgtttgcg cttccgtcgt tgaagaggaa gttcactact tcccaactgt tgatgtttgc 2282
190 catgctgttg actgctgccg gtcagattat tcgtgtcgct ggacctgctt cgctgttgat 2342
192 ggtcgggtact gtgttcgcga tgtttgcat cggagttacc aatgtgttgc ttccgattgc 2402
194 tgtagggag tattttccgc gtcacgtcgg tggaatgtcg acaacttatc tgggtgtcgtt 2462
196 ccagattgtt caggcacttg ctccgacgct tgccgtgccg atttctcagt gggctacaca 2522
198 tgtggggttg accggttggg ggggtgtcgt cggttcgtgg gcgctgctgg ggttggttgc 2582
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204 gtttacttcg tttgcgacgt atatactcat gggttttatg ccgcagatgg taggtgatcc 2762
206 aaagaattca aaaagcttct cgagagtact tctagagcgg ccgcggggcc 2811
209 <210> SEQ ID NO: 2
210 <211> LENGTH: 550
211 <212> TYPE: PRT
212 <213> ORGANISM: Corynebacterium glutamicum
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218 Thr Gln Val Trp Gln Asp Leu Thr Asp His Tyr Ser Asn Phe Gln Ala
219               20               25               30
221 Thr Thr Leu Arg Glu Leu Phe Lys Glu Glu Asn Arg Ala Glu Lys Tyr
222               35               40               45
224 Thr Phe Ser Ala Ala Gly Leu His Val Asp Leu Ser Lys Asn Leu Leu
225   50               55               60
227 Asp Asp Ala Thr Leu Thr Lys Leu Leu Ala Leu Thr Glu Glu Ser Gly
228   65               70               75               80
230 Leu Arg Glu Arg Ile Asp Ala Met Phe Ala Gly Glu His Leu Asn Asn
231               85               90               95
233 Thr Glu Asp Arg Ala Val Leu His Thr Ala Leu Arg Leu Pro Ala Glu
234               100              105              110
236 Ala Asp Leu Ser Val Asp Gly Gln Asp Val Ala Ala Asp Val His Glu
237   115              120              125
239 Val Leu Gly Arg Met Arg Asp Phe Ala Thr Ala Leu Arg Ser Gly Asn
240   130              135              140
242 Trp Leu Gly His Thr Gly His Thr Ile Lys Lys Ile Val Asn Ile Gly
243 145              150              155              160
245 Ile Gly Gly Ser Asp Leu Gly Pro Ala Met Ala Thr Lys Ala Leu Arg
246               165              170              175
248 Ala Tyr Ala Thr Ala Gly Ile Ser Ala Glu Phe Val Ser Asn Val Asp
249               180              185              190
251 Pro Ala Asp Leu Val Ser Val Leu Glu Asp Leu Asp Ala Glu Ser Thr
252               195              200              205
254 Leu Phe Val Ile Ala Ser Lys Thr Phe Thr Thr Gln Glu Thr Leu Ser
255   210              215              220
257 Asn Ala Arg Ala Ala Arg Ala Trp Leu Val Glu Lys Leu Gly Glu Glu
258 225              230              235              240
260 Ala Val Ala Lys His Phe Val Ala Val Ser Thr Asn Ala Glu Lys Val
261               245              250              255
263 Ala Glu Phe Gly Ile Asp Thr Asp Asn Met Phe Gly Phe Trp Asp Trp
264               260              265              270
266 Val Gly Gly Arg Tyr Ser Val Asp Ser Ala Val Gly Leu Ser Leu Met
267               275              280              285
269 Ala Val Ile Gly Pro Arg Asp Phe Met Arg Phe Leu Gly Gly Phe His
270   290              295              300
272 Ala Met Asp Glu His Phe Arg Thr Thr Lys Phe Glu Glu Asn Val Pro
273 305              310              315              320
275 Ile Leu Met Ala Leu Leu Gly Val Trp Tyr Ser Asp Phe Tyr Gly Ala

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276          325          330          335
278 Glu Thr His Ala Val Leu Pro Tyr Ser Glu Asp Leu Ser Arg Phe Ala
279          340          345          350
281 Ala Tyr Leu Gln Gln Leu Thr Met Glu Thr Asn Gly Lys Ser Val His
282          355          360          365
284 Arg Asp Gly Ser Pro Val Ser Thr Gly Thr Gly Glu Ile Tyr Trp Gly
285          370          375          380
287 Glu Pro Gly Thr Asn Gly Gln His Ala Phe Phe Gln Leu Ile His Gln
288 385          390          395          400
290 Gly Thr Arg Leu Val Pro Ala Asp Phe Ile Gly Phe Ala Arg Pro Lys
291          405          410          415
293 Gln Asp Leu Pro Ala Gly Glu Arg Thr Met His Asp Leu Leu Met Ser
294          420          425          430
296 Asn Phe Phe Ala Gln Thr Lys Val Leu Ala Phe Gly Lys Asn Ala Glu
297          435          440          445
299 Glu Ile Ala Ala Glu Gly Val Ala Pro Glu Leu Val Asn His Lys Val
300          450          455          460
302 Val Pro Gly Asn Arg Pro Thr Thr Thr Ile Leu Ala Glu Glu Leu Thr
303 465          470          475          480
305 Pro Ser Ile Leu Gly Ala Leu Ile Ala Leu Tyr Glu His Thr Val Met
306          485          490          495
308 Val Gln Gly Val Ile Trp Asp Ile Asn Ser Phe Asp Gln Trp Gly Val
309          500          505          510
311 Glu Leu Gly Lys Gln Gln Ala Asn Asp Leu Ala Pro Ala Val Ser Gly
312          515          520          525
314 Glu Glu Asp Val Asp Ser Gly Asp Ser Ser Thr Asp Ser Leu Ile Lys
315          530          535          540
317 Trp Tyr Arg Ala Asn Arg
318 545          550

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322 <210> SEQ ID NO: 3

323 <211> LENGTH: 462

324 <212> TYPE: DNA

325 <213> ORGANISM: Corynebacterium glutamicum

327 <400> SEQUENCE: 3

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329 gaaatttact ggggtgagcc tggcacaaat ggccagcacg ctttcttcca gctgatccac 120
330 cagggcactc gccttggtcc agctgatttc attggtttcg ctcttccaaa gcaggatctt 180
331 cctgccggtg agcgcaccat gcatgacctt ttgatgagca acttcttcgc acagaccaag 240
332 gttttggctt tcggttaagaa cgctgaagag atcgctgcgg aagggtgcgc acctgagctg 300
333 gtcaaccaca aggtcgtgcc aggtaatcgc ccaaccacca ccattttggc ggaggaaactt 360
334 accccttcta ttctcgggtg gttgatcgct ttgtacgaac acaccgtgat ggttcagggc 420
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338 <210> SEQ ID NO: 4

339 <211> LENGTH: 2160

340 <212> TYPE: DNA

341 <213> ORGANISM: Corynebacterium glutamicum

343 <220> FEATURE:

344 <221> NAME/KEY: CDS

345 <222> LOCATION: (327)..(2063)

VERIFICATION SUMMARY

DATE: 11/12/2002

PATENT APPLICATION: US/10/091,342

TIME: 10:35:59

Input Set : A:\pto.vsk.txt

Output Set: N:\CRF4\11122002\J091342.raw

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L:12 M:270 C: Current Application Number differs, Replaced Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date